

# Sequential Monte Carlo algorithms for agent-based models of disease transmission

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## **Abstract**

Agent-based models of disease transmission involve stochastic rules that specify how a number of individuals would infect one another, recover or be removed from the population. Common yet stringent assumptions stipulate interchangeability of agents and that all pairwise contact are equally likely. Under these assumptions, the population can be summarized by counting the number of susceptible and infected individuals, which greatly facilitates statistical inference. We consider the task of inference without such simplifying assumptions, in which case, the population cannot be summarized by low-dimensional counts. We design improved particle filters, where each particle corresponds to a specific configuration of the population of agents, that take either the next or all future observations into account when proposing population configurations. Using simulated data sets, we illustrate that orders of magnitude improvements are possible over bootstrap particle filters. We also provide theoretical support for the approximations employed to make the algorithms practical.

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